Search notes

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L5	1888	optical and sequence and (strecth or elongate) and probe	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 13:01
L4	1	optical and sequecne and (strecth or elongate) and probe	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 13:01
L3	2456657	optical ans sequecne and (strecth or elongate) and probe	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 13:01
L2	20	"6054327"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 13:01
L1	17	"6045327"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 12:24
S65	2	"6927065"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 12:23
S79	3	"200113088"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 09:52

EAST Search History

S78	0	PCT near3 "22253"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 09:52
S77	0	PCT/US00/22253	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 09:52
S73	7	"6,767,731"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 09:52
S76	1	"086087" and microparticles	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 09:27
S75	53	"086087"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 09:27
S74	8	"086887"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 09:27
S71	2	"20030059822"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/08 09:01

EAST Search History

S72	7	"6,767,731"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 16:27
S70	3	2003/0059822	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 16:20
S69	24	"5376526"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 16:20
S68	14	S67 and two	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 15:28
S67	14	S66 and complementary	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 13:28
S66	14	bensimon.in. and stretch	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 13:24
S64	2	"20030036067"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 11:17

EAST Search History

S63	2	"20050153284"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 11:16
S62	1	roulon.in. and optical	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 11:15
S61	0	roulon.in. and laminar	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:46
S60	10	tegenfeldt.in. and austin.in.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:46
S59	13	tegenfeldt.in.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:35
S58	65	(optical same sequenc$3) and laminar and stretch and (probe same complementary)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:34
S57	20	(dna same molecule same probe same microscopy) and laminar	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:27

EAST Search History

S56	414	(dna same molecule same probe same microscopy)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:14
S55	7	(gene same engine).clm. and restriction	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:13
S54	22	(gene same engine).clm.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:12
S53	4	gene adj engine	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 09:02
S52	12	liepmann.in. and dorian.in.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/05/07 08:59
S51	12	liepmann.in. and dorian.in.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	OR	ON	2007/05/07 08:58

Scan as search notes

the confinement and detection of fluorescence-labeled DNA nucleotides is also described.

L11 ANSWER 5 OF 5 DISSABS COPYRIGHT (C) 2007 ProQuest Information and Learning Company; All Rights Reserved on STN

ACCESSION NUMBER: 96:14145 DISSABS Order Number: AAI9605253
TITLE: ISOLATION AND CHARACTERIZATION OF QCR9 THE NUCLEAR GENE ENCODING THE 7.3 KDA SUBUNIT 9 OF THE SACCHAROMYCES CEREVISIAE BC(1) COMPLEX (UBIQUINOL, CYTOCHROME C)
AUTHOR: PHILLIPS, JOHN DEARBORN [PH.D.]
CORPORATE SOURCE: DARTMOUTH COLLEGE (0059)
SOURCE: Dissertation Abstracts International, (1991) Vol. 56, No. 10B, p. 5476. Order No.: AAI9605253. 156 pages.
DOCUMENT TYPE: Dissertation
FILE SEGMENT: DAI
LANGUAGE: English
ENTRY DATE: Entered STN: 19960306
Last Updated on STN: 19960306

AB The ubiquinol-cytochrome c oxidoreductase from the yeast Saccharomyces cerevisiae is composed of nine subunits and is located in the inner mitochondrial membrane. Cloning and sequencing of the nuclear gene encoding subunit 9 (QCR9) of the $bc\sb1$ complex have revealed that the gene encodes a protein of 66 amino acids with a predicted molecular weight of 7.3 kDa. The gene contains an intron of 213 bp which separates the initial methionine from the remainder of the coding sequence. This initial methionine is cleaved from the precursor protein on import into the mitochondria.

The protein encoded by QCR9 has a 39% identity to a protein purified from the beef heart complex, and has a 56% similarity to the bovine protein if amino acid substitutions are considered. Secondary structure predictions indicate that the protein has a transmembranous a-helical stretch where all of the identical residues between the yeast and bovine proteins lie on the same face of the helix.

Strains of yeast have been constructed in which the coding region for QCR9 has been replaced with a selectable marker. These yeast strains are unable to grow on non-fermentable carbon sources at 37$\sp\circ$C. The ubiquinol-cytochrome c oxidoreductase activity of these deletion strains is, at most, 5% that of wild type.

The subunit composition of the $bc\sb1$ complex from the deletion strains indicates that there is drastic loss in the amount of Rieske iron-sulfur protein (ISP), when examined by Western blot analysis. The remaining subunits of the complex appear to be present in the predicted stoichiometric ratio. The optical absorption spectrum from a qcr9 deletion strain shows an altered cytochrome b peak, the characteristic peak at 562 nm is greatly reduced.

The intron in QCR9 has a sequence which has a high degree of homology to a sequence in the intron of COX4. The sequence is identical in 18 out of 29 nucleotides. Genomic replacement of an intronless copy of QCR9 has no phenotypic effect on the yeast, however there is an approximate 50% reduction in the expression of QCR9 specific message when the cells are grown on a non-fermentable carbon source.

=> d his

(FILE 'HOME' ENTERED AT 12:58:33 ON 08 MAY 2007)

FILE 'MEDLINE, AGRICOLA, CABA, CAPLUS, BIOSIS, DISSABS, EMBASE, SCISEARCH' ENTERED AT 12:58:48 ON 08 MAY 2007

L1 9 OPTICAL SEQUENCING
L2 4 DUP REM L1 (5 DUPLICATES REMOVED)
L3 137 OPTICAL AND SEQUENCE AND STRETCH
L4 58 DUP REM L3 (79 DUPLICATES REMOVED)
L5 0 L4 AND (HYBRIDIZE)

L6	3	L4 AND (OLIGONUCLEOTIDE)
L7	0	L4 AND ELONGATE
L8	2	L4 AND LINEAR
L9	9	OPTICAL SEQUENCING
L10	13	OPTICAL AND SEQUENCING AND STRETCH
L11	5	DUP REM L10 (8 DUPLICATES REMOVED)